SEQUENCE LISTING

<110> Patrice Jacques Marie PELLERIN
Bruno BLONDIN
Jean-Marie SABLAYROLLES
Carole GUILLAME

<120> YEAST STRAINS WITH IMPROVED FRUCTOSE FERMENTATION CAPACITY

<130> 4662-194 / 21568USWO

<140> US 10/582,987
<141> 2004-12-20

<150> PCT/EP2004/014577
<151> 2004-12-20

<150> EP 03078992.9
<151> 2003-12-19

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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
        35                  40                  45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
    50                  55                  60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65                  70                  75                  80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
                85                  90                  95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
            100                 105                 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
        115                 120                 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
    130                 135                 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
145                 150                 155                 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
                165                 170                 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
            180                 185                 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
        195                 200                 205
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Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
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Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225                 230                 235                 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
                245                 250                 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
            260                 265                 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
        275                 280                 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
    290                 295                 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305                 310                 315                 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
                325                 330                 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
            340                 345                 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
        355                 360                 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
    370                 375                 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val
385                 390                 395                 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn
                405                 410                 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
            420                 425                 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
        435                 440                 445

Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
    450                 455                 460

Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr
465                 470                 475                 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
                485                 490                 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
            500                 505                 510
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Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
        515                 520                 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
    530                 535                 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
545                 550                 555                 560

Lys Lys Met Phe Gly Lys Lys
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<210> 27
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<213> Artificial Sequence

<220>
<223> mutated HXT3 protein

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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro
            20                  25                  30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
        35                  40                  45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
    50                  55                  60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65                  70                  75                  80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
                85                  90                  95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
            100                 105                 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
        115                 120                 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
    130                 135                 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
145                 150                 155                 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
                165                 170                 175
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Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
            180                 185                 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
        195                 200                 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
    210                 215                 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225                 230                 235                 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
                245                 250                 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
            260                 265                 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
        275                 280                 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
    290                 295                 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305                 310                 315                 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
                325                 330                 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
            340                 345                 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
        355                 360                 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
    370                 375                 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val
385                 390                 395                 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn
                405                 410                 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
            420                 425                 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
        435                 440                 445

Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
    450                 455                 460

Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr
465                 470                 475                 480
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Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
                485                 490                 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
            500                 505                 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
        515                 520                 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
    530                 535                 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
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Lys Lys Met Phe Gly Lys Lys
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<210> 30
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated HXT3 protein II

<400> 30

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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro
20 25 30

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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
        35                  40                  45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
    50                  55                  60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65                  70                  75                  80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
                85                  90                  95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
            100                 105                 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
        115                 120                 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
    130                 135                 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
145                 150                 155                 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
                165                 170                 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
            180                 185                 190

Ala Pro Lys Glu Met Arg Gly Ala Leu Val Ser Cys Tyr Gln Leu Met
        195                 200                 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
    210                 215                 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225                 230                 235                 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
                245                 250                 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
            260                 265                 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
        275                 280                 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
    290                 295                 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305                 310                 315                 320

Arg Thr Met Ile Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
                325                 330                 335
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Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
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Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
        355                 360                 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
    370                 375                 380

Asn Cys Leu Met Trp Gly Ala Val Gly Met Val Cys Cys Tyr Val Val
385                 390                 395                 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Gln Asn Asn
                405                 410                 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
            420                 425                 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
        435                 440                 445

Val Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
    450                 455                 460

Ala Thr Ala Ala Asn Trp Ile Trp Gly Phe Leu Ile Gly Phe Phe Thr
465                 470                 475                 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
                485                 490                 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
            500                 505                 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
        515                 520                 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
    530                 535                 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
545                 550                 555                 560

Lys Lys Met Phe Gly Lys Lys
                565
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